SEQUENCE LISTING

<110> PRUSSAK, CHARLES E.
KIPPS, THOMAS J.
CANTWELL, MARK J.

<120> NOVEL CHIMERIC TNF LIGANDS

<130> 041673-2092

<140> 10/006,305
<141> 2001-12-06

<160> 8

<170> PatentIn Ver. 3.2

<210> 1
<211> 771
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Chimeric DNA construct comprising Domain IV of hTNFa linked to Domains I, II, and III of hCD154

<400> 1
atgatcgaaa catacaacca aacttctccc cgatctgcgg ccactggact gcccatcagc 60
atgaaaattt ttatgtattt acttactgtt tttcttatca cccagatgat tgggtcagca 120
ctttttgctg tgtatcttca tagaaggctg gacaagatag aagatgaaag gaatcttcat 180
gaagattttg tattcatgaa aacgatacag agatgcaaca caggagaaag atccttatcc 240
ttactgaact gtgaggagat taaaagccag tttgaaggct ttgtgaagga tataatgtta 300
aacaaagagg agacgaagaa agatgaggat cctgtagccc atgttgtagc aaaccctcaa 360
gctgaggggc agctccagtg gctgaaccgc cgggccaatg ccctcctggc caatggcgtg 420
gagctgagag ataaccagct ggtggtgcca tcagagggcc tgtacctcat ctactcccag 480
gtcctcttca agggccaagg ctgcccctcc acccatgtgc tcctcaccca caccatcagc 540
cgcatcgccg tctcctacca gaccaaggtc aacctcctct ctgccatcaa gagccctgc 600
cagagggaga ccccagaggg ggctgaggcc aagccctggt atgagcccat ctatctggga 660
ggggtcttcc agctggagaa gggtgaccga ctcagcgctg agatcaatcg gcccgactat 720
ctcgactttg cggagtctgg gcaggtctac tttggaatca ttgctctgtg a 771

<210> 2
<211> 580
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Chimeric DNA construct comprising Domain IV of hTNFa linked to Domains I, II, and III of hCD70

<400> 2
atgccggagg agggttcggg ctgctcggtg cggcgcaggc cctatgggtg cgtcctgcgg 60
gctgctttgg tcccattggt cgcgggcttg gtgatctgcc tcgtggtgtg catccagcgc 120
ttcgcacagg ctgcggatcc tgtagcccat gttgtagcaa accctcaagc tgaggggcag 180
ctccagtggc tgaaccgccg ggccaatgcc ctcctggcca atggcgtgga gctgagagat 240
aaccagctgg tggtgccatc agagggcctg tacctcatct actcccaggt cctcttcaag 300

ggccaaggct gcccctccac ccatgtgctc ctcacccaca ccatcagccg catcgccgtc 360
tcctaccaga ccaaggtcaa cctcctctct gccatcaaga gcccctgcca gagggagacc 420
ccagaggggg ctgaggccaa gccctggtat gagcccatct atctgggagg ggtcttccag 480
ctggagaagg gtgaccgact cagcgctgag atcaatcggc ccgactatct cgactttgcg 540
gagtctgggc aggtctactt tggaatcatc gctctgtgaa 580

<210> 3
<211> 837
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Chimeric DNA construct comprising Domain IV of hTNFa linked to Domains I, II, III of hFasL

<400> 3
atgcagcagc ccttcaatta cccatatccc cagatctact gggtggacag cagtgccagc 60
tctccctggg cccctccagg cacagttctt ccctgtccaa cctctgtgcc cagaaggcct 120
ggtcaaagga ggccaccacc accaccgcca ccgccaccac taccacctcc gccgccgccg 180
ccaccactgc ctccactacc gctgccaccc ctgaagaaga gagggaacca cagcacaggc 240
ctgtgtctcc ttgtgatgtt tttcatggtt ctggttgcct tggtaggatt gggcctgggg 300
atgtttcagc tcttccacct acagaaggag ctggcagaac tccgagagtc taccagccag 360
atgcacacag catcatcttt ggagaagcaa gcggatcctg tagcccatgt tgtagcaaac 420
cctcaagctg aggggcagct ccagtggctg aaccgccggg ccaatgccct cctggccaat 480
ggcgtggagc tgagagataa ccagctggtg gtgccatcag agggcctgta cctcatctac 540
tcccaggtcc tcttcaaggg ccaaggctgc ccctccaccc atgtgctcct cacccacacc 600
atcagccgca tcgccgtctc ctaccagacc aaggtcaacc tcctctctgc catcaagagc 660
ccctgccaga gggagacccc agaggggggct gaggccaagc cctggtatga gcccatctat 720
ctgggagggg tcttccagct ggagaagggt gaccgactca gcgctgagat caatcggccc 780
gactatctcg actttgcgga gtctgggcag gtctactttg gaatcattgc tctgtga 837

<210> 4
<211> 813
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Chimeric DNA construct comprising Domain IV of hTNFa linked to Domains I, II, and III of hTRAIL

<400> 4
atggctatga tggaggtcca ggggggaccc agcctgggac agacctgcgt gctgatcgtg 60
atcttcacag tgctcctgca gtctctctgt gtggctgtaa cttacgtgta ctttaccaac 120
gagctgaagc agatgcagga caagtactcc aaaagtggca ttgcttgttt cttaaaagaa 180
gatgacagtt attgggaccc caatgacgaa gagagtatga acagcccctg ctggcaagtc 240
aagtggcaac tccgtcagct cgttagaaag atgattttga gaacctctga ggaaaccatt 300
tctacagttc aagaaaagca acaaaatatt tctcccctag tgagagaaag aggtcctcag 360
agagtagcgg atcctgtagc ccatgttgta gcaaaccctc aagctgaggg gcagctccag 420
tggctgaacc gccgggccaa tgccctcctg gccaatggcg tggagctgag agataaccag 480
ctggtggtgc catcagaggg cctgtacctc atctactccc aggtcctctt caagggccaa 540
ggctgccccct ccacccatgt gctcctcacc cacaccatca gccgcatcgc cgtctcctac 600
cagaccaagg tcaacctcct ctctgccatc aagagccccct gccagaggga gaccccagag 660
ggggctgagg ccaagccctg gtatgagccc atctatctgg gaggggtctt ccagctggag 720
aagggtgacc gactcagcgc tgagatcaat cggcccgact atctcgactt tgcggagtct 780
gggcaggtct actttggaat cattgctctg tga 813

<210> 5
<211> 256
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Chimeric TNFa
polypeptide encoded by the DNA sequence of SEQ ID NO:1

<400> 5

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Met Ile Glu Thr Tyr Asn Gln Thr Ser Pro Arg Ser Ala Ala Thr Gly
  1               5                  10                  15

Leu Pro Ile Ser Met Lys Ile Phe Met Tyr Leu Leu Thr Val Phe Leu
             20                  25                  30

Ile Thr Gln Met Ile Gly Ser Ala Leu Phe Ala Val Tyr Leu His Arg
         35                  40                  45

Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu His Glu Asp Phe Val
     50                  55                  60

Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser Leu Ser
 65                  70                  75                  80

Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe Val Lys
                 85                  90                  95

Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Asp Glu Asp Pro Val
            100                 105                 110

Ala His Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu
        115                 120                 125

Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp
    130                 135                 140

Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln
145                 150                 155                 160

Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr
                165                 170                 175

His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu
            180                 185                 190

Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala
        195                 200                 205

Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln
    210                 215                 220

Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr
225                 230                 235                 240

Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
                245                 250                 255
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<210> 6
<211> 192
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Chimeric TBFa
polypeptide encoded by the DNA sequence of SEQ ID NO:2

<400> 6
Met Pro Glu Glu Gly Ser Gly Cys Ser Val Arg Arg Arg Pro Tyr Gly
1 5 10 15

Cys Val Leu Arg Ala Ala Leu Val Pro Leu Val Ala Gly Leu Val Ile
20 25 30

Cys Leu Val Val Cys Ile Gln Arg Phe Ala Gln Ala Ala Asp Pro Val
35 40 45

Ala His Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu
50 55 60

Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp
65 70 75 80

Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln
85 90 95

Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr
100 105 110

His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu
115 120 125

Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala
130 135 140

Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln
145 150 155 160

Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr
165 170 175

Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
180 185 190

<210> 7
<211> 278
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Chimeric TNFa
polypeptide encoded by the DNA sequence of SEQ ID NO:3

<400> 7

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Met Gln Gln Pro Phe Asn Tyr Pro Tyr Pro Gln Ile Tyr Trp Val Asp
  1               5                  10                  15

Ser Ser Ala Ser Ser Pro Trp Ala Pro Pro Gly Thr Val Leu Pro Cys
             20                  25                  30

Pro Thr Ser Val Pro Arg Arg Pro Gly Gln Arg Arg Pro Pro Pro Pro
         35                  40                  45

Pro Pro Pro Pro Pro Leu Pro Pro Pro Pro Pro Pro Pro Pro Leu Pro
     50                  55                  60

Pro Leu Pro Leu Pro Pro Leu Lys Lys Arg Gly Asn His Ser Thr Gly
 65                  70                  75                  80

Leu Cys Leu Leu Val Met Phe Phe Met Val Leu Val Ala Leu Val Gly
                 85                  90                  95

Leu Gly Leu Gly Met Phe Gln Leu Phe His Leu Gln Lys Glu Leu Ala
            100                 105                 110

Glu Leu Arg Glu Ser Thr Ser Gln Met His Thr Ala Ser Ser Leu Glu
        115                 120                 125

Lys Gln Ala Asp Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu
    130                 135                 140

Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn
145                 150                 155                 160

Gly Val Glu Leu Arg Asp Asn Glu Leu Val Val Pro Ser Glu Gly Leu
                165                 170                 175

Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser
            180                 185                 190

Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr
        195                 200                 205

Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg
    210                 215                 220

Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr
225                 230                 235                 240

Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu
                245                 250                 255

Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr
            260                 265                 270

Phe Gly Ile Ile Ala Leu
        275
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<210> 8
<211> 270
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Chimeric TNFa
polypeptide encoded by the DNA sequence of SEQ ID NO:4

<400> 8

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Met Ala Met Met Glu Val Gln Gly Gly Pro Ser Leu Gly Gln Thr Cys
  1               5                  10                  15

Val Leu Ile Val Ile Phe Thr Val Leu Leu Gln Ser Leu Cys Val Ala
             20                  25                  30

Val Thr Tyr Val Tyr Phe Thr Asn Glu Leu Lys Gln Met Gln Asp Lys
         35                  40                  45

Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser Tyr
     50                  55                  60

Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser Pro Cys Trp Gln Val
 65                  70                  75                  80

Lys Trp Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr Ser
                 85                  90                  95

Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser Pro
            100                 105                 110

Leu Val Arg Glu Arg Glu Pro Gln Arg Val Ala Asp Pro Val Ala His
        115                 120                 125

Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg
    130                 135                 140

Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln
145                 150                 155                 160

Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu
                165                 170                 175

Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr
            180                 185                 190

Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser
        195                 200                 205

Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala
    210                 215                 220

Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu
225                 230                 235                 240

Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp
                245                 250                 255

Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
            260                 265                 27
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